Amendments to the Specification:

Page 13, delete the paragraph at lines 22-38, and insert the following revised paragraph:

Mature human MP52 having the amino acid sequence shown in SEQ ID NO 1 (hereinafter, unmodified mature human MP52) and methionine oxidized mature human MP52 having the amino acid sequence of SEQ ID NO 5 were separated by using reverse phase HPLC on the basis of a difference between retention times of both proteins. Oxidization increased a hydrophilic property of the proteins and retention time methionine oxidized mature human MP52 on the reverse phase HPLC becomes faster than that of unmodified mature human MP52. The conditions of separation are as follows. For column, ~~Nucleosil~~ NUCLEOSIL™ 5-C18-300 column (4.6 mm I.D. X 150 mm, silica material having a particle size of 5 microns, a carbon content of 18% and a pore size of 300 Å, GL Science Corp.) was used at the flow rate of 1.3 ml per minute at 45°C: absorbance at 214 nm and 280 nm were measured to detect peaks. For solvent, water containing 0.05% TFA as solution A and acetonitrile containing 0.05% TFA as solution B were used. Elution of proteins were performed with a linear gradient of solution B from 25% to 45% for 80 minutes using an HPLC pump, HP1050

Page 14, delete the paragraph at lines 20-38, and insert the following revised paragraph:

First, lyophilized unmodified mature human MP52 and methionine oxidized mature human MP52 were dissolved in 8 M urea – 0.2 M ammonium bicarbonate – 2 mM EDTA (pH 8.5) at the final concentration of 1 mg/ml, and 50-fold molar excess of dithiothreitol (DTT) to the cysteine residue was added and reacted at 50°C for 30 minutes. To this solution, 250-fold molar excess of monoiodoacetamide to the cysteine residue was added and reacted for 30 minutes with shading to yield S-carboxymethylated unmodified mature human MP52 and S-carboxymethylated methionine oxidized mature human MP52. Digestion of these proteins was performed by adding trypsin. After four-fold dilution of this solution with water to make the final urea concentration of 2 M, at the weight ratio of 1/50 to the proteins at 37°C for 18 hours, the trypsin digestion was applied to the reverse phase HPLC column to separate all fragments. The conditions of separation are as follows. ~~Nucleosil~~ NUCLEOSIL™ 5-C18-300 column (4.6 mm I.D. X 150 mm, silica material having a particle size of 5 microns, a carbon content of 18% and a pore size of 300 Å, GL Science Corp.) was used for separation at the flow rate of 1.3 ml per minute at 45°C; absorbance at 214 nm was measured

Page 15, delete the paragraph at lines 15-24, and insert the following revised paragraph:

Hydrolysis was performed in a vapor of 6 N HCl containing 0.1% phenol at 110°C for 21 hours by using PICO. TAG. WORK STATION™ (RP-HPLC for

amino acid analysis) (Waters). Following this step, the amino acid composition analysis was carried out by PTC method by using Amino acid standard H (Pierce) as a standard amino acid. PTC-amino acids were separated by reverse phase HPLC using HPLC pump (model 510; Waters), a Wakopak WS-PTC (4.0 mm I.D. X 200 mm; Wako Pure Chemicals), and solvents of PTC amino acids eluent A and PTC amino acids eluent B (both Wako Pure Chemicals).